Application No. : 10/613,053 Confirmation No.: 6718

Applicant: : Imamura
Filed: : July 7, 2003
Group Art Unit: 1638

Examiner: : FOX, David T.

For : Protein Involved in Restoration of Cytoplasmic Male Sterility to Fertility and Gene Encoding the Protein and

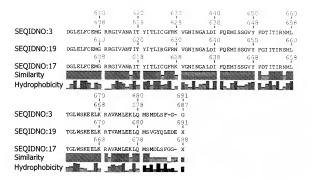
Gene

Docket No. : 54-05A Customer No. : 23713

APPENDIX A and APPENDIX B

	1 10	2.0	3.0	4,0	50	6,5
	1 10	2,0	30	38	4.8	5.8
SEQIDNO:3	MLARVCGFKC	SSSPAESAAR	LFCTRS IRDT	LAKASGES	CE AGF GGES L	KLOSGFHEIK
	1 10	2,0	3,0	4,0	59	69
SEQIDNO:19	MLARVCGFKC	SSSPAVSAAR	LFCTRS IRDT	LAKASRDGES	CEAGFGGESL	KLQSGFHEIK
-	1 10	2.0	3.0	3,8	4.8	5.8
SEQIDNO:17	MLA RVCG FKC	SSSPAESAAR	LFCTRS IRDT	LAKASGES	CE AGFGGES L	KLQSGFHEIK
Similarity						
Hydrophobicity				2.2	الطوا	
,,,	7.0	80	9.0	10	120	1.20
	10	70	90	10.	, 110	140
CEOIDNO.3	OT DESTRU	/°	00	98	108	118
SEQIDNO:3	GLEDAIDLES	DMLRSRPLPS	VV DFCK LMGV	VVRMERP DLV	ISLYQKMERK	QIRCDIYSFN
SEQIDNO:19	70	3,0		10	110	120
SEQIDIVO.19	GLEDAIDLES	DMLRSRPLPS	VV DFCK LMGV	VVRMKRP DVV	IS LHK KMEMR	RIPCDAYSFN
SEQIDNO:17	GLEDAIDLES	DMLRSRPLPS	VV DFCK LMGV	20	100	119
Similarity	GLEDAIDLES	DMLRSRPLPS	VVDFCKLMGV	VVRMERP DLV	ISLYQKMERK	QIRCDIYSFN
		-				
Hydrophobicity						
	1.30) 140	150	160	170	180
	125	3 138	149	158	168	178
SEQIDNO:3	ILIKCFCSCS	KLPFALSTFG	KITKLGLHPD	VVTFTTL LHG	LCVEDRVSE A	LDF FHQM FET
	130	140	150	160	170	190
SEQIDNO:19	ILIKCFCSCS	KLPFALSTFG	KLTKLGLHPD	VVTFTTLLHG	LC VEN RGSE A	LNLFHQMFET
	128	3 138	148	3 158	168	178
SEQIDNO:17	ILI KCFCSCS	KLPFALSTFG	KLTKLGLHPD	VVTFTTLLHG	LCVEDRVSE A	LNLFHQMFET
Similarity			-			
Hydrophobicity			LHL			
	190	200	210	220	230	240
	188	198	208	218	228	238
SEQIDNO:3	TCRPNVVTFT	TLMNGLCREG	RI VEAVALLD	RMME DGLOPT	OITYGTIVDG I	MCKKGDTVSA
	190	200	210	220	230	240
SEQIDNO:19	TCRPNVVTFT	TLMNGLCREG	RIVEAVALLD	RMME DGL QPT	QITYGTIVDG	MCK KGDTVSA
-	188	198	208	218	228	238
SEQIDNO:17	TCR PNVV TFT	TLMNGLCREG	RIVEAVALLD	RMME DGL QPT	QITYGTIVDG	MCKKGDTVSA
Similarity						
Hydrophobicity				-L-	Land	
	25:	260	270	280	290	300
	248	258	288	278	288	299
SEQIDNO:3	LNLLRKMEEV	SHITPNVVIV	SATINGICKO	CRHSDAON' F	TEMORKSTED I	DLFTYNSMIV
SEQIDITO.S	250	260	170 ICKD	28(190	300
SEQIDNO:19	LNLLRKMEEV	SHITPNVVIV	SATIDSLCKD	GRHS DSQNLF	TEMORKGIED	DLFTYNCMIN
410,10,13	248	258	268	278	288	208
SEQIDNO:17	LNLLRKMEEV	SHIIPNVVIY	SAIIDSLCKD	GRHS DAONLF	TEMOEKGIFP	DLFTYNSMIV
Similarity						
Hydrophobicity			-E E	W	- 5	

	310	320	330	340	350	360
SEQIDNO:3	308	318 EOLLOEMLE RKI	328	338	348	358
SEQIDINO:S	GFCSSGRWSD A 310	320 320	33C	NAFVKE GKFF 340	EAEELY DEMI 350	LPRGIIP 360
SEQIDNO:19	GFCSSGRWID A	EQLLQEMLE RKI		NAFVKE GKFF		PRGIIP
SEQIDNO:17	GFCSSGRWSD A	318 EOLLOEMLE RKI	328 SPDVVTY NALI	338 NAFVKE GKFF	348 EAEELY DEMI	358
Similarity	GECSSGRWSD A	EQUIDORNUE RA	SPDVVII NALI	NAFVKE GKFF	EAEELY DEMI	LPRGIIP
Hydrophobicity			TT.	7 1		7,5
	370	380	390	400	410	429
	368	378	388	398	108	418
SEQIDNO:3	NTITYSSMID G	FCKQNRLDA AEF	MFYLMAT KGCS	PNLITF NTLI	DGYCGA KRIE	DDGMELL 420
SEQIDNO:19	NTITYSSMID G	0,1	MFYLMPT KGCS	PDVFTF NTLI	DGYRGA KRID	DOGMELL
-	369	378	388	398	408	419
SEQIDNO:17	NTITYSSMID G	FCKQNRLDA AEF	MFYLMAT KGCS	PNLITF NTLI	DGYCGA KRID	DOGMELL
Similarity Hydrophobicity					-3	
Пушторновісісу	430	440	450	460	470	480
	428	438	448	458	468	478
SEQIDNO:3	HEMTETGLVA D	TTTYNTLIH GFY		LQEMIS SGLC	PDIVTC DTLL	DGL CDN
SECTION C:10	430	440	450	460	470	480
SEQIDNO:19	HEMTEAGLVA N	IVTYNTLIH GFO 438	QVGDLTA ALDL 448	LHEMIS SGVC: 458	PNVVTC STLL 468	DGLCDN 478
SEQIDNO:17	HEMTETGLVA D	TTYNTLIH GFY	LVGDLNA ALDL	LQEMIS SGLC	PDIVTC DTLL	DGLCDN
Similarity						
Hydrophobicity	490	500				
	488	498	510 508	520 518	530 528	540 538
SEQIDNO:3		1	1		1	LYEEMP
	490	500	510	520	530	540
SEQIDNO:19	GKL KDAWELF K	VMQKSKMDL DAS	HPFNGVE PDVQ	TYNILI SGLII 518	NEGKFL EAEE 508	LYKEMP 538
SEQIDNO:17	GKL KDALEMF K	MOKSKKOL DAS	HPFNGVE PDVO	F .		LYEEMP
Similarity						
Hydrophobicity						
	550	560	570	580	590	600
SEQIDNO:3	548 HRGIVPDTIT Y	558 SSMIDGLCK OSF	568 LDEATOM FDSM	578 GSKSFS PNVV	588 FFTTLI NGYC	598 KAGRVD
3EQIDIVO.3	550	560	570	580	590	600
SEQIDNO:19	HRGIVPDTIT Y	SSMIDGLCK QSR	LDEATOM FDSM	GSKSFS PNVV		KAGRVD
SEQIDNO:17	548 HRGIVPDTIT Y:	5ក្ន SSMIDGLCK OSR	568	578	588	598
Similarity	INGIALDIII I	POLIT DOP CV (72)	LDEATQM FDSM	GSKSFS PNVV	FTTLI NGYC	KAGRVD
Hydrophobicity			يرا بديا			L



	1 10	20	30	45	5 [4	
	1 1	2.0	30	47	5(6,0	70
seqidno2	ATGTTGGCTA	GGGTTTGTGG	ATTCAAGTGT	TCTTCTTCTC	CTGCTGAGTC	TGC GGCT AGA	TTGTTCTGTA
coaidno 10	1 Imammaaami	20	" (momm omm omo	om com omom o	maa aaam s as	mmommomom)
seqiuiloto	ATGTTGGCTA	GGGTTTGTGG	ATTCAAGTGT 30	ACTICITATION 6/	CTGCTGTGTC	TGCGGCTAGA	TTGTTCTGTA
segidno16	ATGTTGGCTA	GGGTT TGT GG	1	TCTTCTTCTC	CTGCTGAGTC	TGC GGCT AGA	TTGTTCTGTA
Similarity							
,	8 (90	100	0 17	0 12	0 13	0 140
	80	1			106 11		
seqidno2	CGAGATCGAT	TCGTGATACT		CAAGC	-GGAGAGAGT	TGC GAAG CAG	G TTT TGGA GG
	8.0	9,0	100			0 13	0 140
seqidno18	CGAGATCGAT	TCGTGATACT	CTGGCC AAGG	CAAGCAGGGA	TG GAG AGAG T		GTTTTGGAGG
	8(1	100		106 11	4 12	4 134
	CGA GATC GAT	TCGTGATACT	CTGGCC AAGG	CAAGC	-GGAG AGAG T	TGCGAAGCAG	GTTTTGGAGG
Similarity					7		
	1.5	0 1.6	170	0 18	0 19	0 20	0 210
	24	4 15	1 16.	4 17	4 18	4 19	4 201
seqidno2	AGA GAGTTTG	AAGCTGCAAA	GTGGGTTTCA	TGAAATCAAA	GGTTTAGAGG	ATGCGATTGA	
	16	0 16	170	18	0 19	9 39	0 210
seqiano18	AGA GAGTTTG	AAGCTGCAAA	GTGGGTTTCA 4 1.6	TGAAATCAAA	GGTTT AGAGG	ATG CGAT TGA	TTTGTTCAGT 4 204
segidno16	AGA GAGTTTG	AAGCTGCAAA	GTGGGTTTCA	TGAAATCAAA	GG TTT AGAGG	ATG CGAT TGA	TTTCTTCACT
Similarity	AGAGAGTTIG	AAGCT GCAAA	GIGGGIIICA	TORRATCARA	GGTTTAGAGG	ATOCOATTOA	TITGTICAGE
Jirimaricy	22	0 23	240	25	0 26	0 27	0 280
	21					- 1	1
segidno2	GACATGCTTC	GATCTCGTCC	1	GTGGTTGATT	1		1
ocqianoz	22	0 23	240	25		27	0 280
seaidno18	GAC ATGC TTC	GATCTCGTCC	TTTACCTTCT	GTGGTTGATT	TCTGTAAATT	GATGGGTGTG	G TGG TGAG GA
	2.1	4 32-	4 23	4 24	4 25	4 26	4 274
	GAC ATGCTTC	GATCTCGTCC	TTTACCTTCT	GTGGTTGATT	TCTGTAAATT	GATGGGTGTG	GTGGTGAGAA
Similarity							-
	29	0 30	310	32	0 33	0 34	0 350
	28	4 29			4 32	1 33	1 341
seqidno2	TGGAACGCCC	GGATCTTGTG		ATCA GAA GAT	GGAAAGG	AAACAGATTC	GATGTGATAT
	2.9	0 30		32	0 33	33	7 347
seqidno18	TGA AACG CCC	GGATGTTGTG	ATTTCTCTCC	ATAAGAAGAT	GGAAA TGCGG	CGCATTC	CATGTGATGC
	29	a 29.	4 30	1 37	4 32	33	341
	TGGAACGCCC	GGATC TTG TG	ATTTCTCTCT	ATCA GAA GAT	GG AAA G G	AAACAGA TTC	GATGTGATAT
Similarity							

Regidno ATACAGCTTC ANATYTCTGA TANAMISTIT CTGCAGCTGC TCTAAGCTGC CCTTTGCTTT GTGTACATTT		36	0 37	0 36	0 394	401	9 41	0 420
Regidno2 ATACAGCTTC AATATTCTGA TANAATGTTT CTCCAGCTGC TCTAGACTCT CCTTTGCTTT GTCTACATTT		1						
Pagidino18 ATACAGCTTC ANTATTCTGA TANAGCTTT CTGCARCTGC CCTTAGCTTT GTTT-ACACTTT	segidno2	ATA CAGC TTC	A ATAT TCT GA	TAAAATGTTT		,	CCTTTGCTTT	1
Sqidno16 ATACAGCTTC ATATTTCGA TANANTGTT CTGCAGCTGC TCTAAGCTC CCTTGCTTT GTCTACATTT		35	7 36			- 1	7 40	7 417
ATTACAGETTC ANTATTECTA TANANTSTT CTGCAGCTG TCTAAGCTC CCTTTGCTT GTCTACATT	seqidno18	ATACAGCTTC			CTGC AGC TGC	TCTAAGCTGC	CCTTTGCTTT	GTCTACATTT
		35	1 36.	1 37	1 38:	i 39:	1 40	1 411
#430		ATA CAGC TTC	AATATTCTGA	TAAAATGTTT	CTGC AGC TGC	TCTAAGCTCC	CCTTTGCTTT	GTCTACATTT
A	Similarity			-		•		
A		43	1			- 1	1	1
427		42	į	1	1 45	1 46	1 47	1 481
Peqidino18 GSTAAGCTCA CCAAGCTTGG ACTCCACCCT GATGTTGTTA CCTTCACCAC CCTTCTCCAC GGATTGTGTG	seqidno2	GGT AAGA TCA	CCAAGCTTGG		GATGTTGTTA	CCTTCACCAC	CCTGCTCCAT	GGATTATGTG
421		14	43	' i	/ 45	7 49	′ 4/	1 487
STAGET ACCEPT & CCARGETT G ACTOCACCOT GATGTTGTA CCTTCACCAC CCTGCTCCAC GGATTGTCCC GIMIlarity STAGE STAGET	seqianora	GGTAAGCTCA					CCTTCTCCAC	GGATTGTGTG
	eaidno16	T T				. 1	CCTCCTCCAC	CCATTCTCCC
S S S S S S S S S S		GOTANGE TEX	CGMGC11GG	ACTCCACCCT	GATGITGITA	COTTORCORC	CCT GCTCCAC	SGAT 1616C6
Page	Jirmaney	5.0	0 51	0 52	0 53	5.4	5.5	0 560
		. 1					1	1
497 597 517 527 537 547 557	egidno2	1		1		AA TOTTO A	1	1
	cqianoz	49			7 52	7 53	7 54	
491 591 511 521 531 541 551	eaidno18	TGGAAAA TAG	GGGTTCTGAA	GCTTTGAATT	TGTTTCATCA	AATGT TTGAA	ACGRCATGTA	
STATE STAT								
\$70		4.9	1 50	1 51:	1 52	i 53:	1 54	1 551
eqidno2 cotaacctrta caccattra transcerta transcereta t	eqidno16	ī	1				1 54 ACGACATGTA	1
Pagidino2 CGTAACCTTC ACCACTTTGA TGAACGGTCT TTGCCGCCGAG GGTAGAATTG TGGAAGCGGT AGCTCTGCTT		ī	1				54 ACGACATGTA	1
1		TGGAAGA TAG	GGTTT CTGAA	GCTTTGAATT	TGTTTCATCA	AA TGT TTGA A		G GCC CAAT GT
Peqidino18 CSTARCCTTC ACCACTTTCA TGARGGGTT TTGCCCCGAG GGTAGAATTG TGGARGCGT AGCTCTACTT		TGGAAGA TAG	GGTTTCTGAA 0 58	GCTTTGAATT	TGTTTCATCA	AATGTTTGAA	62	GGCC CAAT GT 0 630
Seqidino16 CETARCETTE ACCACTTTGA TGAAGGGGTT TGCCGGCGGG GGTAGAATTG TGGAAGCGGT AGCTCGGTT	Similarity	TGGAAGA TAG 57	GGTTT CTGAA 0 531 1 57	GCTTTGAATT 0 59	TGTTTCATCA 0 600 1 591	AATGTTTGAA 0 61: 1 60:	0 62 1 61	GGCC CAAT GT 0 630 1 601
	Similarity seqidno2	TGGAAGA TAG 57 56 CGT AACCTTC	GGTTT CTGAA 0 58 1 57 A CCACTTT GA 7 57	GCTTTGAATT 0 596 ! 58 TGAACGGTCT	TGTTTCATCA 0 639 1 59 TTGCCGCGAG	AATGTTTGAA	0 62 1 61	GGCC CAAT GT 0 630 3 621 AGCT CTGCTT
	Similarity seqidno2	TGGAAGA TAG 57 56 CGT AACCTTC 56 CGT AACCTTC	GGTTTCTGAA C 58 57 ACCACTTTGA 7 57 ACCACTTTGA	GCTTTGAATT 0 59 1 58 TGAACGGTCT 7 58 TGAACGGTCT	TGTTTCATCA 0 600 1 599 TTGCCGCGAG 7 599 TTGCCGCGAG	AATGTTTGAA 0 61; 1 60; GGTAGAATTG GGTAGAATTG	O 62 1 61 TCGAAGCCGT 7 61 TCGAAGCCGT	GGCC CAAT GT 0 630 1 621 AGCT CTGCTT 7 627 AGCT CTACTT
640 650 660 670 680 690 700	Similarity seqidno2 seqidno18	TGGAAGA TAG 57 56 CGT AACCTTC 56 CGT AACCTTC 56	GGTTTCTGAA 0 58 57 ACCACTTTGA 7 57 ACCACTTTGA 1 57	GCTTTGAATT 0 59 1 58 TGAACGGTCT 7 58 TGAACGGTCT 1 58	TGTTTCATCA 0 600 1 590 TTGCCGCGAG 7 590 TTGCCGCGAG 1 590	AATGTTTGAA 0 611 1 60 GGTAGAATTG GGTAGAATTG GGTAGAATTG	O 62 1 61 TCGAAGCCGT 7 61 TCGAAGCCGT	GGCC CAAT GT 0 630 1 621 AGCT CTGC TT 7 627 AGCT CTAC TT 1 621
eqidno2 GATCGGATGA TGGAAGATGG TCTCCAGCCT ACCCAGATTA CTTATGGAAC AATCGTAGAT GGGATGTGTA 637 647 657 667 677 687 697 eqidno18 GATCGGATGA TGGAAGATGG TCTCCAGCCT ACCCAGATTA CTTATGGAAC AATCGTAGAT GGGATGTGTA 631 641 651 661 671 691 691 eqidno16 GATCGGATGA TGGAAGATGG TCTCCAGCCT ACCCAGATTA CTTATGGAAC AATCGTAGAT GGGATGTGTA	Similarity Seqidno2 Seqidno18 Seqidno16	TGGAAGA TAG 57 56 CGT AACCTTC 56 CGT AACCTTC 56	GGTTTCTGAA 0 58 57 ACCACTTTGA 7 57 ACCACTTTGA 1 57	GCTTTGAATT 0 59 1 58 TGAACGGTCT 7 58 TGAACGGTCT 1 58	TGTTTCATCA 0 600 1 590 TTGCCGCGAG 7 590 TTGCCGCGAG 1 590	AATGTTTGAA 0 611 1 60 GGTAGAATTG GGTAGAATTG GGTAGAATTG	O 62 1 61 TCGAAGCCGT 7 61 TCGAAGCCGT	GGCC CAAT of 0 630 1 601 AGCT CTGC TT 7 627 AGCT CTAC TT 1 621
eqidno2 GATCGGATGA TGGAAGATGG TCTCCAGCCT ACCCAGATTA CTTATGGAAC AATCGTAGAT GGGATGTGTA 637 647 657 667 67 67 687 697 eqidno18 GATCGGATGA TGGAAGATGG TCTCCAGCCT ACCCAGATTA CTTATGGAAC AATCGTAGAT GGGATGTGTA 651 661 671 691 691 eqidno16 GATCGGATGA TGGAAGATGG TCTCCAGCCT ACCCAGATTA CTTATGGAAC AATCGTAGAT GGGATGTGTA 651 661 671 671 691 691 691 691 691 691 691 691 691 69	Similarity Seqidno2 Seqidno18 Seqidno16	TGGAAGATAG 57 56 CGTAACCTTC 56 CGTAACCTTC	GGTTTCTGAA C 531 57 ACCACTTTGA 7 57 ACCACTTTGA 1 57 ACCACTTTGA	O 5991 1 58 TGAACGGTCT	0 631 1 59 TTGCCGCGAG 7 59 TTGCCGCGAG 1 59 TTGCCGCGAG	AA TGTTTGAA 1 60: GGTAGAATTG GGTAGAATTG GGTAGAATTG GGTAGAATTG	CONTROL OF THE PROPERTY OF T	GGCC CAAT GT 0 630 1 621 AGCT CTGC TT 627 AGCT CTACTT 1 621 AGCT CTGC TT
637 647 657 667 677 687 697 eqidno18 GATCGGATGA TGGAAGGG TCTCCAGCCT ACCCAGATTA CTTATGGAAC AATCGTAGAT GGGATGTGTA 631 641 651 661 671 691 691 eqidno16 GATCGGATGA TGGAAGATGG TCTCCAGCCT ACCCAGATTA CTTATGGAAC AATCGTAGAT GGGATGTGTA	Similarity seqidno2 seqidno18 seqidno16	TGGAAGA TAG 57 56 CGTAACCTTC 56 CGTAACCTTC 56 CGTAACCTTC	GGTTTCTGAA C 58 2 57 ACCACTTTGA 7 57 ACCACTTTGA 1 57 ACCACTTTGA 0 65	0 59 ! 58 TGAACGGTCT 7 58: TGAACGGTCT 1 58 TGAACGGTCT	0 626 1 59 TTGCCGCGAG 7 59 TTGCCGCGAG 1 59: TTGCCGCGAG	AA TGTTTGAA 0 61: 1 60: GGTAGAATTG GGTAGAATTG GGTAGAATTG GGTAGAATTG GGTAGAATTG	O 62 1 61 TCGAAGC CGT 7 61 TCGAAGC CGT 1 61 TCGAAGC CGT	GGCCCAATGT 0 630 1 621 AGCTCTGCTT 7 627 AGCTCTACTT 1 621 AGCTCTGCTT 1 700
eqidno18 gatoggatga toggagatgg totocagott acceagatta ottatoggado aatogtagat gogatotota 631 641 651 661 671 691 691 eqidno16 gatoggatga toggagatgg totocagott acceagatta ottatoggago aatogtagat gogatotota	Similarity seqidno2 seqidno18 seqidno16 similarity	TGGAAGA TAG 57 56 CGTAACCTTC 56 CGTAACCTTC 64 64 63	GGTTTCTGAA C 58 57 ACCACTTTGA ACCACTTTGA 1 57 ACCACTTTGA 0 65 1 64	GCTTTGAATT 0 59 ! 58 TGAACGGTCT 7 58 TGAACGGTCT 1 58 TGAACGGTCT 0 66 1 65	TGTTTCATCA 0 601 1 59 TTGCCGCGAG 7 59 TTGCCGCGAG 1 59 TTGCCGCGAG 0 67 1 66	AA TGT TTGAA 1 60: GGTAGAATT G	CONTROL OF THE PROPERTY OF T	GGCCCAATGT 0 630 1 631 AGCTCTGCTT 7 627 AGCTCTACTT 1 621 AGCTCTGCTT 1 621 0 700 1 691
631 641 651 661 671 691 691 eqidno16 gateggatga teggaagatga tetecageet acceagatta ettatggaac aategtagat gegaatgteta	Similarity seqidno2 seqidno18 seqidno16 Similarity	TGGAAGA TAG 57 56 CGTAACCTTC 56 CGTAACCTTC 64 63 GATCGGA TGA	GGTTTCTGAA C 581 1 57 ACCACTTTGA 7 57 ACCACTTTGA 1 57 ACCACTTTGA 0 651 1 644 TGGGAAGATGG	GCTTTGAAT 0 59 1 58 TGAACGGTCT 7 58 TGAACGGTCT 1 58 TGAACGGTCT 0 66 1 65 TCTCCAGCCT	TGTTTCATCA 0 62i 1 59i TTGCCGCGAG 1 59i TTGCCGCGAG 1 59i TTGCCGCGAG 1 66i ACCCAGATTA	AATGTTTGAA 1 60' 1 60' 2 GGTAGAATTG 1 60' 3 GGTAGAATTG 2 GGTAGAATTG 3 GGTAGAATTG 4 60' CTTATGGAAC	CONTROL OF THE PROPERTY OF THE	GGCC CAAT GT 0 630 1 631 7 621 7 627 AGCT CTACTT 1 621 AGCT CTGCTT 0 700 1 691 GGGA TGTGTA
eqidno16 gatcggatga tggaagatgg tctccagcct acccagatta cttatggaac aatcgtagat gggatgtgta	Similarity seqidno2 seqidno18 seqidno16 Similarity seqidno2	TGGAAGATAG 57 56 CGTAACCTTC 56 CGTAACCTTC 56 GGTAACCTTC 64 63 GATCGGATGA 63	GGTTTCTGAA C 52: 2 57: ACCACTTTGA 7 57: ACCACTTTGA 1 64: TGGAAGATGG 7 64:	GCTTTGAATT 0 59 1 58 TGAACGGTCT 7 58 TGAACGGTCT 1 58 TGAACGGTCT 1 65 1 65 TCTCCAGCCT 7 66	0 691 1 599 TTGCCGGGAG 7 597 TTGCCGGGAG 1 599 TTGCCGGGAG 0 671 1 666 ACCCAGATTA 7 666	AA TGTTTGA A 1 60: 6 60: 7 60' 6 GGTAGAATTG 1 60: 6 GGTAGAATTG 2 68: 1 67: CTTATGGAAC 7 67'	0 62 1 61 TCGAAGCCGT 7 61 TCGAAGCCGT 1 61 TCGAAGCCGT 0 69 1 68 AATCGTAGAT 7 68	GGCCCAATGT 0 630 AGCTCTGCTT AGCTCTACTT AGCTCTACTT AGCTCTGCTT AGCTCTGCTT C 700 T 700 T 697 GGATGTCTA 7 697
	Similarity seqidno2 seqidno18 seqidno16 Similarity seqidno2	TGGAAGATAG 57 56 CGTAACCTTC 56 CGTAACCTTC 56 GGTAACCTTC 64 63 GATCGGATGA 63	GGTTTCTGAA C 52: 2 57: ACCACTTTGA 7 57: ACCACTTTGA 1 64: TGGAAGATGG 7 64:	0 591 1 58 TGAACGGTCT 7 58 TGAACGGTCT 1 58 TGAACGGTCT 1 58 TGAACGGTCT 1 58 TGAACGGTCT 1 65 TCTCCAGCCT TCTCCAGCCT TCTCCAGCCT	0 691 1 599 TTGCCGGGAG 7 597 TTGCCGGGAG 1 599 TTGCCGGGAG 0 671 1 666 ACCCAGATTA 7 666	AA TGTTTGA A 1 60: 6 60: 7 60' 6 GGTAGAATTG 1 60: 6 GGTAGAATTG 2 68: 1 67: CTTATGGAAC 7 67'	0 62 1 61 TCGAAGCCGT 7 61 TCGAAGCCGT 1 61 TCGAAGCCGT 0 69 1 68 AATCGTAGAT 7 68	GGCCAATGT 0 630 0 630 1 621 AGCTCTGCTT 7 627 AGCTCTACTT 1 621 AGCTCTGCTT 0 700 1 691 GGGATGTGTA 7 697 GGGATGTGTA
ATTIMITY	seqidno2 seqidno18 seqidno16 Similarity seqidno2 seqidno18	TGGAAGATAG 57 56 CGTAACCTTC 56 CGTAACCTTC 64 63 GATCGGATGA 63 GATCGGATGA 63	GGTTTCTGAA C 52 57 ACCACTTTGA 7 ACCACTTTGA 1 57 ACCACTTTGA 0 65 1 64 TGGAAGATGG 7 64 TGGAAGATGG 1 64	GCTTTGAATT 1 59 1 59 1 59 TGAACGGTCT 7 58 TGAACGGTCT 1 58 TGAACGGTCT 0 66 1 65 TCTCCAGCCT 7 65 TCTCCAGCCT 1 65	TGCTTCATCA 0 60 0 60 1 59 TTGCCGCGAG 7 59 TTGCCGCGAG 1 59 TTGCCGCGAG 0 67 1 66 ACCCAGATTA 1 66 ACCCAGATTA 1 66	AA TGT TTGAA 1 60: GGTAGAATTG 1 60: GGTAGAATTG 2 60: GGTAGAATTG 4 67: CTTATGGAAC 1 67: CTTATGGAAC 1 67:	0 62 1 61 TCGAAGC CGT TCGAAGC CGT TCGAAGC CGT TCGAAGC CGT 1 62 1 68 AAT CGTAGAT AAT CGTAGAT 1 69	GGCCAATGT 630 1 631 AGCTCTGCTT 7 627 AGCTCTACTT 1 621 AGCTCTGCTT
	seqidno2 seqidno18 seqidno16 Similarity seqidno2 seqidno18 seqidno16	TGGAAGATAG 57 56 CGTAACCTTC 56 CGTAACCTTC 64 63 GATCGGATGA 63 GATCGGATGA 63	GGTTTCTGAA C 52 57 ACCACTTTGA 7 ACCACTTTGA 1 57 ACCACTTTGA 0 65 1 64 TGGAAGATGG 7 64 TGGAAGATGG 1 64	GCTTTGAATT 1 59 1 59 1 59 TGAACGGTCT 7 58 TGAACGGTCT 1 58 TGAACGGTCT 0 66 1 65 TCTCCAGCCT 7 65 TCTCCAGCCT 1 65	TGCTTCATCA 0 60 0 60 1 59 TTGCCGCGAG 7 59 TTGCCGCGAG 1 59 TTGCCGCGAG 0 67 1 66 ACCCAGATTA 1 66 ACCCAGATTA 1 66	AA TGT TTGAA 1 60: GGTAGAATTG 1 60: GGTAGAATTG 2 60: GGTAGAATTG 4 67: CTTATGGAAC 1 67: CTTATGGAAC 1 67:	0 62 1 61 TCGAAGC CGT TCGAAGC CGT TCGAAGC CGT TCGAAGC CGT 1 62 1 68 AAT CGTAGAT AAT CGTAGAT 1 69	GGCCAATGT 630 1 631 AGCTCTGCTT 7 627 AGCTCTACTT 1 621 AGCTCTGCTT

	70	1 71	1 72	1 75	1 74	1 75	1 761
seqidno2	AGA AGGG AGA	TACTGTGTCT	GCACTGAATC	TGCTGAGGAA	GA TGG AGGA G	GTGAGCCACA	TCATACCCAA
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	77	1 78	1 79	1		1 82	1
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coaldno16	TOTTOTA ATC	TATAGTGC AA	TC ATTG ATAG		GACGGACGTC	ATA GCGA TGC	ACAAAATCTT
Similarity	IGITGIARIC	I RIRGIOCAL	Territorine	CCTTTOTTER	CHCCCACCTC	- A	-
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	92 1 90	0 93	AGGAAT CTTT 0 941 9 92 GCGACG CGGA	0 95 9 93	0 96 9 94 CAAGAAATGT	0 97 9 95 TAGAAAGGAA	0 980 9 969 GATCAGCCCT
Similarity seqidno2	92 90 TTGTAGCTCT 91	0 93 9 91 GGTAGATGGA 5 92	AGGAAT CTTT 0 94 9 92 GC GACGCGGA 5 93	0 95 9 93 GCAGTTGTTG 5 94	0 96 9 94 CAAGA AATGT 5 95	0 97 9 95 TAGAAAGGAA 5 96	0 930 9 969 GATCAGCCCT 5 975
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Similarity seqidno2 seqidno18 seqidno16	92 90 TTGTAGCTCT 91 TTGTAGCTCT	0 93 9 91 GGTAGATGGA 5 92	AGGAAT CTTT 0 94 9 92 GC GACGCGGA 5 93 TC GACGCGGA 9 92	0 95 9 93 GCAGTTGTTG 5 94 GCAGTTGTTG	0 96 9 94 CAAGA AATGT 5 95 CAAGA AATGT 9 94	0 97 9 95 TAGAAAGGAA 5 96 TAGAAAGGAA 9 95	930 9 969 GATCAGCCCT 5 975 GATCAGCCCT 9 969
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Similarity seqidno2 seqidno18 seqidno16 Similarity	92 90 TTGTAGCTCT 91 TTGTAGCTCT 90 TTGTAGCTCT	0 93 9 91 GGTAGATGGA 5 92 GGTAGATGGA 9 91 GGTAGATGGA 0 1,0	AGGAATCTTT 0 94 9 92 GCGACGCGGA 5 93 TCGACGCGGA 9 92 GCGACGCGGA 0 1,0 9 99	0 95 9 93 GCAGTTGTTG 5 94 GCAGTTGTTG 9 93 GCAGTTGTTG	0 96 9 94 CAAGA AATGT 5 95 CAAGA AATGT 9 94 CAAGA AATGT	0 97 9 95 TAGAAAGGAA 5 96 TAGAAAGGAA 9 95 TAGAAAGGAA	0 980 9 969 GATCAGCCCT 5 975 GATCAGCCCT 9 969 GATCAGCCCT
Similarity seqidno2 seqidno18 seqidno16	92 90 TTGTAGCTCT 91 TTGTAGCTCT 90 TTGTAGCTCT	0 93 9 91 GGTAGATGGA 5 92 GGTAGATGGA 9 91 GGTAGATGGA 0 1,0	AGGAATCTTT 0 94 9 92 GCGACGCGGA TCGACGCGGA 9 92 GCGACGCGGA	0 95 9 93 GCAGTTGTTG 5 94 GCAGTTGTTG 9 93 GCAGTTGTTG	0 96 9 94 CAAGA AATGT 5 95 CAAGA AATGT 9 94 CAAGA AATGT	0 97 9 95 TAGAAAGGAA 5 96 TAGAAAGGAA 9 95 TAGAAAGGAA 30 1,0	9 969 GATCAGCCCT 5 975 GATCAGCCCT 9 969 GATCAGCCCT 40 1,050
seqidno2 seqidno18 seqidno16 Similarity seqidno2	92 90 TTGTAGCTCT 91 TTGTAGCTCT 90 TTGTAGCTCT 99 97 GATGTTGTAA	0 93 9 91 6GTAGATGGA 9 91 6GTAGATGGA 9 91 6GTAGATGGA 9 91 6GTAGATGGA 9 98 6 CTTATAAATGC 5 99	AGGAATCTTT 0 944 9 92; GCGACGCGGA 5 93; TCGACGCGGA 9 92; GCGACGCGGA 1,00 9 99; TTTGATCAAT 5 1,00	0 95 9 93 GCAGTTGTTG 5 94 GCAGTTGTTG 9 93 GCAGTTGTTG	0 96 9 94 CAAGA AATGT 5 95 CAAGA AATGT 9 94 CAAGA AATGT	0 97 9 95 TAGAAAGGAA 5 96 TAGAAAGGAA 9 95 TAGAAAGGAA 30 1,0 10 1,0 GTTCTTTCAG 25 1,0	G 980 9 969 GATCAGCCT 5 975 GATCAGCCT 9 969 GATCAGCCT 40 1,050 29 1,039 GCTGAAGAAT
seqidno2 seqidno18 seqidno16 Similarity seqidno2	92 90 TTGTAGCTCT 91 TTGTAGCTCT 90 TTGTAGCTCT 99 97 GATGTTGTAA	0 93 9 91 GGTAGATGGA 5 92 GGTAGATGGA 9 91 GGTAGATGGA 0 1,0	AGGAATCTTT 0 944 9 92; GCGACGCGGA 5 93; TCGACGCGGA 9 92; GCGACGCGGA 1,00 9 99; TTTGATCAAT 5 1,00	0 95 9 93 GCAGTTGTTG 5 94 GCAGTTGTTG 9 93 GCAGTTGTTG 10 1,7 9 1,0 GCATTGTCA 35 1,0 GCATTTGTCA	0 96 9 94 CAAGAAATGT 5 95 CAAGAAATGT 9 94 CAAGAAATGT 20 1,0 09 1,0 09 1,0 AGGAAGGCAA	0 97 9 95 TAGAAAGGAA 5 96 TAGAAAGGAA 9 95 TAGAAAGGAA 30 1,0 10 1,0 GTTCTTTCAG 25 1,0	0 980 0 969 GATCAGCCCT 5 975 GATCAGCCCT 969 GATCAGCCCT 40 1,050 229 1,039 GCTGAAGGAT 35 1,045
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